

SEQUENCE LISTING

<110> VAISVILA, ROMUALDAS

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CLAUS, TOBY E.

RALEIGH, ELISABETH A.

<120> METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
ENDONUCLEASE

<130> NEB-181

<140>

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<170> PatentIn Ver. 2.0

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<211> 903

<212> DNA

<213> Micrococcus sp.

<220>

<221> CDS

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Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe	
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cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag ccg	144
Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg	
35 40 45	

ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc	192
Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly	
50 55 60	

ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat	240
Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr	

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 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu

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gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg 336
 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu

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gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc 384
 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe

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gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc 432
 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly

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gcg cgc tgc aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg 480
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tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat 528
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175

cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg 576
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185

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ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct 624
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atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg 720
 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu

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gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc 768
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gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta 816
 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val

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atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc 864
 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
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 <213> Micrococcus sp.

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Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
 35 40 45

Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
 50 55 60

Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
 65 70 75 80

Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
 85 90 95

Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
 100 105 110

Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
 115 120 125

Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
 130 135 140

Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
 145 150 155 160

Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp

	165		170		175
Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala					
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Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro					
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Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile					
	210		215		220
Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu					
	225		230		235
Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu					
	245		250		255
Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val					
	260		265		270
Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile					
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<223> Description of Unknown Organism: ENVIRONMENTAL DNA

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1 5 10 15	
acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg	96
Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro	
20 25 30	

cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg	144
Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu	
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ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct	192
Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro	
50 55 60	
ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat	240
Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp	
65 70 75 80	
tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag	288
Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu	
85 90 95	
tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta	336
Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val	
100 105 110	
ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg	384
Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu	
115 120 125	
gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc	432
Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe	
130 135 140	
ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc	480
Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro	
145 150 155 160	
tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt	528
Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val	
165 170 175	
tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa	576
Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln	
180 185 190	
cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc	624
Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala	
195 200 205	
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Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp	
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tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc	768
Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala	
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Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly	
260 265 270	
aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac	864
Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn	
275 280 285	
gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc	912
Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg	
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gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct	960
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305 310 315 320	
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Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile	
325 330 335	
cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa	1056
Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln	
340 345 350	
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Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg	
355 360 365	
ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg	1152
Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu	
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Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr	
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35 40 45

Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
50 55 60

Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
65 70 75 80

Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
85 90 95

Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
100 105 110

Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
115 120 125

Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
130 135 140

Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
145 150 155 160

Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
165 170 175

Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
180 185 190

Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
195 200 205

Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
210 215 220

Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
 225 230 235 240

Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
 245 250 255

Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
 260 265 270

Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
 275 280 285

Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
 290 295 300

Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
 305 310 315 320

Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
 325 330 335

Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
 340 345 350

Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
 355 360 365

Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
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Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
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<223> Description of Unknown Organism: ENVIRONMENTAL DNA

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<222> (1)..(921)

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gcc gac aac atg gaa gtc ctg cga ggg ctt ccg gcg gcg tcc gtg gac	96
Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp	
20 25 30	
ctg atc tac atc gat cct ccg ttc aac acc gga aag gtt cag gag cgc	144
Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg	
35 40 45	
act cag ctc aaa acg gtg cgc tcc gag tgg ggc gat cgc gtc gga ttc	192
Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe	
50 55 60	
cag ggc cgt cgc tac gaa agc atc gtc gtg ggt aag aag cgc ttt acc	240
Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr	
65 70 75 80	
gac ttc ttc gac gac tat ctg gct ttc ctg gaa ccg cgc ctg gtc gaa	288
Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu	
85 90 95	
gcc cat cgt gtt ctg gcg ccg cac ggg tgc ctc tac ttt cac gtc gac	336
Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp	
100 105 110	
tac cgc gag gtg cac tac tgt aag gtc ctt ctt gac ggc atc ttc ggt	384
Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly	
115 120 125	
cgc gag gcc ttt ctc aac gag atc atc tgg gcc tac gat tac ggc ggg	432
Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly	
130 135 140	
cgt ccg aag gac agg tgg cct cct aag cac gac aac atc ctg ctc tac	480
Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr	
145 150 155 160	
gcc aag act ccc ggt cgc cac gtg ttc aat gcg gac gaa atc gag cgc	528
Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg	
165 170 175	
att ccc tac atg gct ccg ggc ctg gtt ggc ccc gaa aag gca gcc cgt	576

Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
 180 185 190

gga aaa ctg cca acc gac acg tgg tgg cat acg atc gtt ccg acc agc 624
 Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
 195 200 205

ggc tcc gag aag acc ggg tat cca acc cag aaa cct tta ggg att ctc 672
 Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
 210 215 220

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 Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
 225 230 235 240

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 Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
 245 250 255

cgg cgt ttc att ctg gtc gat aac cat ccg gag gcc ctc cag gtg atg 816
 Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
 260 265 270

gcc agg cgc ttc gac ggc atc gag ggg atc gaa tgg gtg ggc ttc gat 864
 Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
 275 280 285

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 Pro Thr Gly
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 <213> Unknown

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 Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
 50 55 60
 Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
 65 70 75 80
 Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
 85 90 95
 Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
 100 105 110
 Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
 115 120 125
 Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
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 Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
 145 150 155 160
 Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
 165 170 175
 Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
 180 185 190
 Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
 195 200 205
 Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
 210 215 220
 Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
 225 230 235 240
 Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
 245 250 255
 Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
 260 265 270
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Pro Thr Gly
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<220>
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 Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
 20 25 30
 tgg gtc ggc agc ccg ttc gag tgg atc ctt cgc gtt cca tcc aga acg 144
 Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
 35 40 45
 aag ggc gcg gtc ggt gag ctg ctc gtg agc gaa tgg gct aat gcc aaa 192
 Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
 50 55 60
 ggc ctc cgt gtg aag agg tcg ggg tcc agc gat gcg gac cgc gtg atc 240
 Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
 65 70 75 80
 aac ggg cat cgc atc gag atc aag atg tcg act ttg tgg aag tcc ggc 288
 Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
 85 90 95
 ggc ttc aag ttt cag cag atc cgg gat cag gag tac gac ttt tgc ctc 336
 Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
 100 105 110
 tgc ctt ggg atc agc ccg ttc gaa gtg cac gcg tgg ctg ctg ccc aaa 384
 Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
 115 120 125

gac cta ttg ctt gag tac gtg att ggt cac atg ggt cag cac acc ggc 432
 Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
 130 135 140

gcg agc ggg agc gac act gcg tgg ctg ggg ttc cca gcg gac gag ccg 480
 Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
 145 150 155 160

tat gac tgg atg cgc cct ttc gga ggt cgc tta ggt cac gtc gaa gat 528
 Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
 165 170 175

ctc ctc ctc gcg gcc ggc ccc ggt ccc tac tga 561
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 180 185

<210> 8
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Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
 35 40 45

Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
 50 55 60

Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
 65 70 75 80

Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
 85 90 95

Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
 100 105 110

Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
 115 120 125

Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
 130 135 140

Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
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Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
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Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
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<211> 413

<212> DNA

<213> Escherichia coli

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 ccgggtttttt ttgcgttgaa tttgtcattt tgtgccgtgg tgtttaaac gcacagaata 180
 aattgtcgtg atttcacctt taaaataaaa taaaagaga aaaaaattct ctgtggaagg 240
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 tctttgcagg cactggctga agccgttaat ctgacaacca ccccttgctg gaagcgctg 360
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